OM protein - protein search, using sw model

GenCore version 4.5
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Run on: January 30, 2002, 11:50:30 ; Search time 27.34 Seconds
(without alignments)
72.441 Million cell updates/sec

Title:
Perfect score: 183
Sequence: 1 RRWPWPWKWPLIGGGYDPAPPPPP 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_68:*
2: pir1:*
3: pir2:*
4: pir3:*
  pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	77	42.1	161	2	E48232	cysteine-rich exte
2	71.5	39.1	248	2	S23449	NADH oxidase (H2O2
3	70	38.3	172	2	T27505	hypothetical prote
4	68.5	37.4	221	2	T07176	hypothetical prote
5	68	37.2	142	2	T51039	extensin homolog -
6	68	37.2	196	2	B48232	related to extensi
7	68	37.2	209	2	A48232	cysteine-rich exte
8	68	37.2	969	2	T15446	cysteine-rich exte
9	66.5	36.3	160	2	D42232	hypothetical prote
10	66	36.1	10	2	A36454	cysteine-rich exte
11	66	36.1	1171	2	T17454	trypsin-modulating
12	66	35.5	1662	2	T18540	diaphanous-related
13	64	35.0	148	2	S39906	mofA protein precu
14	64	35.0	534	2	S21961	proline-rich prote
15	64	35.0	650	2	T04487	proline-rich prote
16	64	35.0	691	2	T46676	hypothetical prote
17	64	35.0	1137	2	A86635	hypothetical prote
18	64	35.0	1404	2	E85509	hypothetical prote
19	63	34.4	172	2	D41132	hypothetical prote
20	63	34.4	304	2	A32993	collagen-related p
21	62	33.9	137	2	T22308	transcription fact
22	62	33.9	144	2	JC1222	hypothetical prote
23	62	33.9	502	2	T08776	indolicidin precur
24	62	33.9	584	2	B84668	hypothetical prote
25	62	33.9	776	2	S45495	ethylene-insensiti
26	62	33.9	856	2	T13159	isp4 protein - fis
27	61.5	33.6	445	2	S19990	alpha-amylase (EC
28	61.5	33.6	684	2	A56154	Abl substrate ena
29	61	33.3	106	2	A30996	orf-X protein - si
30	61	33.3	112	1	ASLJX2	vpu protein - huma
31	61	33.3	112	1	ASLJCX	vpu protein - huma
32	61	33.3	112	1	ASLJST	vpu protein - simi
33	61	33.3	112	1	ASLJX3	vpu protein - simi
34	61	33.3	112	1	S12155	vpx protein - huma
35	61	33.3	112	2	S03066	gene X protein - h
36	61	33.3	112	2	S53094	vpx protein - huma
37	61	33.3	140	2	T19083	36K antigen pra
38	61	33.3	249	2	A41497	hypothetical prote
39	61	33.3	282	2	T26635	hypothetical prote
40	61	33.3	473	2	B85187	glycoprotein homol
41	61	33.3	492	2	T21934	hypothetical prote
42	61	33.3	1044	2	S01966	GTPase-activating
43	61	33.3	1353	2	S12155	probable metal bin
44	61	33.3	1424	2	T19157	probable metal bin
45	61	33.3	1585	2	T31611	hypothetical prote

ALIGNMENTS

RESULT 1

E48232
cysteine-rich extensin-like protein 5 precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Nov-2000
C;Accession: E48232
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma
A;Reference number: A48232; MUID:93342083
A;Accession: E48232
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <WUA>
A;Cross-references: GB:L13443; NID:g310930; PIDN:AAA34063.1; PID:g310931
C;Genetics:
A;Gene: CELP-5
C;Superfamily: glutelin
C;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-160/Product: cysteine-rich extensin-like protein 5 #status experimental <MAT>

Query Match 42.1%; Score 77; DB 2; Length 161;
Best Local Similarity 43.8%;
Matches 14; Conservative 2; Mismatches 2; Indels 14; Gaps 3;

```
Qy      3 WPW-------WPW--KWPLIGGGYDPAPPPPPP 26
            |||      |||  ||:||||||||
Db     41 WPWKIPCYLWPFPRWPC-----PSPPPPPP 66
```

RESULT 2

S23449
NADH oxidase (H2O2-forming) (EC 1.6.--) - Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 23-Mar-1993
C;Accession: S23449; S24556
R;Park, H.J.; Kreutzer, R.; Reiser, C.O.A.; Sprinzl, M.
Eur. J. Biochem. 205, 875-879, 1992
A;Title: Molecular cloning and nucleotide sequence of the gene encoding a H(2)O(2)-fo
A;Reference number: S23449; MUID:92249331
A;Accession: S23449
A;Molecule type: DNA
A;Residues: 1-248 <PAR>
A;Accession: S24556
A;Molecule type: protein
A;Residues: 1-32 <PAR1>
A;Cross-references: EMBL:X60110
C;Genetics:
A;Gene: nox
C;Keywords: NAD; oxidoreductase

F;1-248/Product: NADH oxidase (H202-forming) #status experimental <MAT>

Query Match   39.1%; Score 71.5; DB 2; Length 248;
Best Local Similarity 44.1%;
Matches   15; Conservative 0; Mismatches 8; Indels 11; Gaps 3;

Qy   1 RRW-------------PWWPWKWPLIGGGYDPAPPPPP 25
                        ||| ||||||||
Db 167 RSWGFLPTPSPSPWWPWA-TRTCGGL-PLPPPAP 198

RESULT   3
T27505
hypothetical protein ZC168.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27505
R;Berks, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20378
A;Accession: T27505
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-172 <WIL>
A;Cross-references: EMBL:Z70312; PIDN:CAA94385.1; GSPDB:GN00022; CESP:ZC168.5
A;Experimental source: clone ZC168
C;Genetics:
A;Gene: CESP:ZC168.5
A;Map position: 4
A;Introns: 112/3

.Qy
Query Match   38.3%; Score 70; DB 2; Length 172;
Best Local Similarity 68.8%;
Matches   11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy   11 PLIGGGYDPAPPPPP 26
         |||||| ||||||
Db   45 PPCGGGYEAPPPPPP 60

RESULT   4
T07176
extensin homolog - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 17-Nov-2000
C;Accession: T07176
R;Macleod, M.R.
submitted to the EMBL Data Library, December 1997
A;Reference number: Z15977
A;Accession: T07176
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-221 <MAC>
A;Cross-references: EMBL:AJ003220; NID:e1251331; PIDN:CAA06000.1; PID:e1251332
A;Experimental source: cv. Record; swelling stolon
C;Superfamily: glutelin

Query Match   37.4%; Score 68.5; DB 2; Length 221;
Best Local Similarity 36.8%;
Matches   14; Conservative 3; Mismatches 4; Indels 17; Gaps 3;

Qy   3 WPW-------------WPWKWPLIGGGYD--------PAPPPPP 26
         ||| |:| |:||||||
Db   24 WPWEIPCYLPWPFPFP---RPYPCPPPKPRPSPPPPP 58

RESULT   5
T51039
related to extensin precursor [imported] - Neurospora crassa
N;Alternate names: protein B15120.90

C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T51039
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25286
A;Accession: T51039
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <SCH>
A;Cross-references: EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.90
A;Experimental source: BAC clone B15120; strain OR74A
C;Genetics:
A;Gene: NCSP:B15120.90
A;Map position: 6

Query Match   37.28%; Score 68; DB 2; Length 142;
Best Local Similarity 42.9%;
Matches   15; Conservative 3; Mismatches 7; Indels 10; Gaps 2;

Qy   1 RRWP-------------WWPWKWPLIG--GGYDPAPPPPP 25
         ||:| | ||:|| |||||||
Db   87 RRFPLKIRPGSWVPFKFPLTSFFLSSFGPAPPPPP 121

RESULT   6
B48232
cysteine-rich extensin-like protein 2 precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: B48232
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A;Title: Developmental expression of tobacco pistil-specific genes encoding novel ext
A;Reference number: PQ0474; MUID:93005740
A;Accession: PQ0474
A;Molecule type: mRNA
A;Residues: 1-105 <GOL>
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma
A;Reference number: A48232; MUID:93342083
A;Accession: B48232
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-196 <WUA>
A;Cross-references: GB:L13440; NID:g310924; PIDN:AAA34060.1; PID:g310925
A;Experimental source: stigma, style; strain Petit Havana SR1
C;Genetics:
A;Gene: CELP-2
C;Superfamily: glutelin
C;Keywords: cell wall; extracellular matrix; fertilization
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-196/Product: cysteine-rich extensin-like protein 2 #status experimental <MAT>

Query Match   37.28%; Score 68; DB 2; Length 196;
Best Local Similarity 38.7%;
Matches   12; Conservative 1; Mismatches 2; Indels 16; Gaps 2;

Qy   3 WPW-------------WPWKWPLIGGGYDPAPPPPPP 26
         ||| ||||| |
Db   40 WPWEIPCYLTWPFPWP-----------PPPPWP 61

RESULT   7
A48232
cysteine-rich extensin-like protein 1 precursor - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C;Accession: A48232; PQ0475; S24617

R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A;Reference number: A48232; MUID:93342083
A;Accession: A48232
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <WUA>
A;Cross-references: GB:L13439; NID:g310922; PIDN:AAA34059.1; PID:g310923
R;de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A;Title: Developmental expression of tobacco pistil-specific genes encoding novel extens
A;Reference number: PQ0474; MUID:93005740
A;Accession: PQ0475
A;Superfamily: glutelin
A;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
A;Molecule type: mRNA
A;Residues: 39-209 <GOL>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>
F;146/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   37.2%; Score 68; DB 2; Length 209;
Best Local Similarity 38.7%; Pred. No. 0.94;
Matches 12; Conservative 1; Mismatches 2; Indels 16; Gaps 2;

```
Qy    3 WPW-----------WPWKWPLIGGYDPAPPPPP 26
          ||| |||||||||
Db   45 WPWEIPCYLIWPPPWP----------PPPWP 66
```

RESULT 8
T15446
hypothetical protein C07G1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15446
R;Hawkins, J.
A;Reference number: Z18352
A;Description: The sequence of C. elegans cosmid C07G1.
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-969 <HAW>
A;Cross-references: EMBL:U58751; NID:g1326379; PIDN:g1326381; PIDN:AAB00657.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone C07G1
A;Gene: CESP:C07G1.4
A;Genetics:
A;Map position: 4
A;Introns: 110/3; 149/2; 515/1; 564/1; 600/2; 690/2; 755/3; 843/3; 884/3; 940/2

Query Match   37.8%; Score 68; DB 2; Length 969;
Best Local Similarity 55.0%; Pred. No. 4.6;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

```
Qy    7 PWKWPLIGGYDPAPPPPP 26
          |:|| |||||||||
Db  799 PMGLPAVGAGAPPPPPPP 818
```

RESULT 9
D48232
cysteine-rich extensin-like protein 4 precursor - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Nov-2000
C;Accession: D48232
R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A;Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma
A;Reference number: A48232; MUID:93342083
A;Accession: D48232
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-160 <WUA>
A;Cross-references: GB:L13442
A;Note: authors failed to translate the codon GCT for residue 11 as Ala, and GTA for
A;Note: authors translated the codon TCT for residue 60 as Pro, and CCA for residue 1
A;Genetics:
A;Superfamily: glutelin
A;Gene: CELP-4
A;Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-159/Product: cysteine-rich extensin-like protein 4 #status experimental <MAT>

Query Match   36.3%; Score 66.5; DB 2; Length 160;
Best Local Similarity 35.0%; Pred. No. 1;
Matches 14; Conservative 2; Mismatches 5; Indels 3; Gaps 3;

```
Qy    3 WPW-----------WPWKWPLIGGYD-----------PAPPPPP 26
          ||| ||||||||
Db   39 WPWKIPCYLRWPPPFP---RPYPCSPPRPRRPCPPPPPP 75
```

RESULT 10
A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C;Species: Aedes aegypti (yellow fever mosquito)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996
C;Accession: A36454; A61630
A;Residues: 1-10 <BOR>
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A;Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme
A;Reference number: A36454; MUID:9036788B
A;Accession: A36454
A;Molecule type: protein
A;Residues: 1-10 <BOR>
R;Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A;Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating o
A;Reference number: A61630; MUID:93357794
A;Accession: A61630
A;Molecule type: protein
A;Residues: 1-10 <BO2>
A;Note: none of the amino acids is modified
C;Function:
A;Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut
C;Keywords: hormone

Query Match   36.1%; Score 66; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   17 YDPAPPPPPP 26
          ||||||||||
Db    1 YDPAPPPPPP 10
```

RESULT 11
T17454
diaphanous-related formin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17454
R;Tominaga, T.; Sahai, E.; Treisman, R.H.; Alberts, A.S.
submitted to the EMBL Data Library, September 1998
A;Reference number: 218796
A;Accession: T17454
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

A;Residues: 1-1171 <TOM>
A;Cross-references: EMBL:AF094519; NID:g3834629; PID:AAC71771.1
C;Genetics:
A;Gene: Dia2

```
Qy        Query Match    36.1%;    Score 66;  DB 2;  Length 1171;
          Best Local Similarity    62.5%;    Pred. No. 9.3;
          Matches   10;  Conservative   1;  Mismatches   5;  Indels   0;  Gaps   0;

Qy   11 PLIGGGYDPAPPPPPP 26
          | ||||:|:| |||||||
Db  559 PALSGGVPPPPPPPP 574
```

RESULT 12
T18540
mofA protein precursor [imported] - Leptothrix discophora
C;Species: Leptothrix discophora
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2000
C;Accession: T18540
R;Corstjens, P.L.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z18959
A;Accession: T18540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1662 <COR>
A;Cross-references: EMBL:Z25774; NID:e1427784; PID:e267517; PIDN:CAA81037.1
C;Genetics:
A;Note: mofA
F;1-33/Domain: signal sequence #status predicted <SIG>
F;43-1662/Product: mofA protein #status predicted <MAT>

```
Qy        Query Match    35.5%;    Score 65;  DB 2;  Length 1662;
          Best Local Similarity    52.9%;    Pred. No. 17;
     ·    Matches    9;  Conservative   1;  Mismatches   7;  Indels   7;  Gaps   0;

Qy    2 RWPWWPWKWPLIGGGYD 18
          | || ||| |:| |||
Db  490 RWHWGPWFWPVFPAMYD 506
```

RESULT 13
S39206
proline-rich protein V-beta 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
C;Accession: A53118; S39206
R;Courty, Y.; Rosinski-Chupin, I.; Rougeon, F.
J. Biol. Chem. 269, 520-527, 1994
A;Title: A new proline-rich protein precursor expressed in the salivary glands of the ra
A;Reference number: A53118; MUID:94103265
A;Accession: A53118
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-148 <COU>
A;Cross-references: EMBL:X74229; NID:g433616; PIDN:CAA52300.1; PID:g433617
A;Note: submitted to the EMBL Data Library, July 1993
C;Genetics:
A;Gene: VCS-beta
A;Introns: 18/3
C;Superfamily: proline-rich peptide P-B
C;Keywords: glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-148/Product: proline-rich protein V-beta 1 #status predicted <MAT>
F;133,143/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
          Query Match    35.0%;    Score 64;  DB 2;  Length 148;
          Best Local Similarity    62.5%;    Pred. No. 1.8;
          Matches   10;  Conservative   1;  Mismatches   5;  Indels   0;  Gaps   0;
```

```
Qy   11 PLIGGGYDPAPPPPPP 26
          | ||:| | |||||||
Db   56 PHFGPGFGPPPPPPPP 71
```

RESULT 14
S21961
proline-rich protein APG - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S21961
R;Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J
submitted to the EMBL Data Library, August 1991
A;Description: Cloning and characterization of a proline-rich gene expressed specific
A;Reference number: S16748
A;Accession: S21961
A;Molecule type: DNA
A;Residues: 1-534 <ROB>
A;Cross-references: EMBL:X60377; NID:g22598; PID:g22599
C;Genetics:
A;Gene: APG
A;Introns: 256/1; 299/3; 387/3; 470/1

```
Qy        Query Match    35.0%;    Score 64;  DB 2;  Length 534;
          Best Local Similarity    37.5%;    Pred. No. 6.8;
          Matches   12;  Conservative   3;  Mismatches   11;  Indels   6;  Gaps   1;

Qy    1 RRWPW------WPWKWPLIGGGYDPAPPPPPP 26
          | ||:     || |: | |  |:
Db   41 RLWPWPLWPRYPQPWPMPNPPTPDDPSPKVAP 72
```

RESULT 15
T04487
hypothetical protein F8F16.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T04487
R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheisel, J.; M
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15375
A;Accession: T04487
A;Molecule type: DNA
A;Residues: 1-650 <BEV>
A;Cross-references: EMBL:AL021633
A;Experimental source: cultivar Columbia; BAC clone F8F16
C;Genetics:
A;Map position: 4
A;Introns: 337/2; 428/1
A;Note: F8F16.10

```
Qy        Query Match    35.0%;    Score 64;  DB 2;  Length 650;
          Best Local Similarity    68.8%;    Pred. No. 8.3;
          Matches   11;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;

Qy   11 PLIGGGYDPAPPPPPP 26
          | |||||||||||||
Db  106 PPFPGPVDSAPPPPPP 121
```

Search completed: January 30, 2002, 11:50:31
Job time: 125 sec